10/045,400

IN THE CLAIMS

1. (previously presented) A method of diagnosing non-small cell lung cancer (NSCLC) in a human, the method comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human, whereby a lower degree of expression of the gene in the human relative to a normal level of expression of the gene in humans not afflicted with NSCLC is an indication that the human is afflicted with NSCLC.

2-42. (canceled)

2 ~~43~~. (previously presented) The method of claim 1 wherein expression of the gene is assessed *in vitro* in cells obtained from the human.

3 ~~44~~. (previously presented) The method of claim ~~43~~ 2 wherein the cells are obtained from a bronchial lavage.

4 ~~45~~. (previously presented) The method of claim ~~43~~ 2 wherein the cells are epithelial cells.

5 ~~46~~. (previously presented) The method of claim 1 wherein the human does not exhibit a macroscopic clinical symptom of NSCLC.

6 ~~47~~. (previously presented) The method of claim ~~46~~ 5 wherein the symptom is selected from the group consisting of (a) a persistent cough which gets worse over time, (b) constant chest pain, (c) expectoration of blood, (d) shortness of breath, (e) wheezing, (f) hoarseness, (g) recurrent pneumonia, (h) recurrent bronchitis, (i) swelling of the neck and face, (j) loss of appetite, (k) weight loss, and (l) fatigue.

7 ~~48~~. (previously presented) The method of claim 1 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

49. (canceled)

8 50. (previously presented) The method of claim 7 48 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

9 51. (previously presented) The method of claim 8 50 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.

10 52. (currently amended) A method of assessing NSCLC tumorigenesis at an early stage in a human comprising assessing expression of ~~a promoter of~~ the gene encoding DAP-kinase in lung cells of the human, whereby a lower ~~higher~~ degree of expression of the gene is an indication of early-stage tumorigenesis.

11 53. (currently amended) A method of assessing aggressiveness of a NSCLC tumor in a human comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human, whereby a lower ~~higher~~ degree of expression of the gene is an indication that the tumor is aggressive.

12 54. (currently amended) The method of claim 11 53 wherein the tumor is a diagnostic stage I NSCLC tumor.

13 55. (currently amended) The method of claim 11 53 further comprising the step of selecting among methods of treating the NSCLC tumor, wherein a more aggressive treatment is selected if a higher degree of expression is detected.

14 56. (previously presented) A method of assessing the risk that a human will develop NSCLC comprising assessing expression of the gene encoding DAP-kinase in lung cells of the human, wherein a lower degree of expression of the gene in the human relative to a normal level

of expression of the gene in humans not afflicted with NSCLC is an indication that the human is at an increased risk for developing NSCLC.

See Examiner's Amendment 10-17-06

57. (withdrawn) A method of assessing whether a test compound is useful for inhibiting a process selected from the group consisting of (1) NSCLC tumorigenesis, (2) progression of a NSCLC tumor, and (3) aggressiveness of a NSCLC tumor comprising comparing expression of the DAP-kinase gene in the presence of the test compound with expression of the DAP-kinase gene in the absence of the test compound, wherein a lower degree of expression in the presence of the test compound is an indication that the test compound is useful for inhibiting the process.

15 ~~58.~~ (previously presented) The method of claim 52 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

16 ~~59.~~ (previously presented) The method of claim 58 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

17 ~~60.~~ (previously presented) The method of claim 59 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.

18 ~~61.~~ (previously presented) The method of claim 53 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

19 ~~62.~~ (previously presented) The method of claim 61 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

20 ~~63.~~ (previously presented) The method of claim 62 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.

64. (previously presented) The method of claim 56 wherein expression of the gene is assessed by assessing methylation of the gene's promoter.

65. (previously presented) The method of claim 64 wherein methylation is assessed using a first oligonucleotide which specifically hybridizes to a methylated form of the promoter.

66. (previously presented) The method of claim 65 wherein a portion of the promoter is amplified by a polymerase chain reaction using the first oligonucleotide and a second oligonucleotide.